**Molecular Characterization of Breast Invasive Lobular Carcinoma Metastasis to the Ovaries**

**Background:** Invasive lobular carcinoma (ILC) accounts for 5-15% of newly diagnosed breast cancers in US annually. ILC is characterized by small and regular uniform cells with single-file pattern of invasion. These tumors are often estrogen-receptor (ER) and progesterone-receptor (PR) positive, but mostly HER2 negative with less proliferative pattern than invasive ductal carcinoma (IDC). Both subtypes can metastasize to similar sites, however, ILC tend to have a different pattern of metastasis compared to IDC by infiltrating the peritoneum, ovaries, and gastrointestinal system. Data from both metastases and general registries of MWH has shown significant metastasis of ILC to the ovaries when compared to IDC. Other than altered expression of E-cadherin, not much is known about molecular pathways involved in unique ILC metastasis.

**Hypothesis:** The unique biology of ILC drives progression and metastasis that are specific to the ILC subtype. Our goal is to investigate the etiology and unique biology of ILC, with the eventual goal of developing targeted therapeutics.

**Methods:** We performed gene expression analysis between FFPE samples from 19 ovarian metastases (10 ILC, 5 IDC, and 4 mixed) and 7 matched primaries using DESeq2 and edgeR packages. We Identified 802 DE genes with adjusted p-value <0.005 and FC>2 from both paired and unpaired analyses. GSEA analysis was performed to decipher the biological processes involving the differentially expressed genes. Moreover, we identified a new QC parameter to confirm paired samples using SNP identified using GATK package.

**Results/conclusions:** Collectively, preliminary results highlighted *CNTNAP2, CDH3, CLDN11*, and *CNTN1* genes as part of cell adhesion molecule pathway. The analysis also revealed *FGFR4* and *FGF12* involvement in regulation of actin cytoskeleton*. FGF12, CTNNA3, LAMA1, PDGFRA,* and *WNT5A* also appeared as part of KEGG pathways in cancer. Future work will focus more on functional validation of these targets, variant calling, and detection of functional fusions.